

SEQUENCE LISTING

<110> Ruben et al.

<120> Neutrokin-Alpha Binding Proteins And Methods based Thereon

<130> PF524C1

<140> Unassigned

<141> 2002-03-01

<150> 09/533,822

<151> 2000-03-24

<150> 60/188,208

<151> 2000-03-10

<150> 60/126,599

<151> 1999-03-26

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 882

<212> DNA

<213> Homo sapiens

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<222> (1)..(882)

<400> 1

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cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg gtg gct atg aga      96
Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
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tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg ggt acc tgc atg      144
Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
           35               40              45

tcc tgc aaa acc att tgc aac cat cag agc cag cgc acc tgt gca gcc      192
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
           50               55              60

ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc aag ttc tat gac      240
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
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cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga cag cac      288
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His

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Pro	Lys	Gln	Cys	Ala	Tyr	Phe	Cys	Glu	Asn	Lys	Leu	Arg	Ser	Pro	Val															
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aac	ctt	cca	cca	gag	ctc	agg	aga	cag	cgg	agt	gga	gaa	gtt	gaa	aac	384														
Asn	Leu	Pro	Pro	Glu	Leu	Arg	Arg	Gln	Arg	Ser	Gly	Glu	Val	Glu	Asn															
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Asn	Ser	Asp	Asn	Ser	Gly	Arg	Tyr	Gln	Gly	Leu	Glu	His	Arg	Gly	Ser															
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Glu	Ala	Ser	Pro	Ala	Leu	Pro	Gly	Leu	Lys	Leu	Ser	Ala	Asp	Gln	Val															
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gcc	ctg	gtc	tac	agc	acg	ctg	ggg	ctc	tgc	ctg	tgt	gcc	gtc	ctc	tgc	528														
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				165					170					175																
tgc	ttc	ctg	gtg	gcg	gtg	gcc	tgc	ttc	ctc	aag	aag	agg	ggg	gat	ccc	576														
Cys	Phe	Leu	Val	Ala	Val	Ala	Cys	Phe	Leu	Lys	Lys	Arg	Gly	Asp	Pro															
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tgc	tcc	tgc	cag	ccc	cgc	tca	agg	ccc	cgt	caa	agt	ccg	gcc	aag	tct	624														
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 35 40 45
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50 55 60
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65 70 75 80
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85 90 95
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
 165 170 175
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
 180 185 190
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
 195 200 205
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
 210 215 220
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
 225 230 235 240
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
 245 250 255
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
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 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
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 tctcccgagc tcctgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240

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ggctgaatgg caaggagtag aagtgcaagg tctccaacaa agccctccca acccccatcg 360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC aactacaaga 540
ccacgcctcc cgtgctggac tccgacggct ctttcttctt ctacagcaag ctcaccgtgg 600
acaagagcag gtggcagcag gggAACgtct tctcatgctc cgtgatgcat gaggtctctg 660
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<222> (1)..(5)
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<220>
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